

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:45:51 ; Search time 40 Seconds
(without alignments)
610.976 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPGWFLGYLILGVA.....GVYTNLCRFTWIKTVQAS 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	567.5	41.5	253	A53968	serine proteinase
2	563.5	41.2	260	I56559	neuropsin - mouse
3	524	38.3	261	S45303	tissue kallikrein
4	515	37.6	244	A44284	tissue kallikrein
5	510.5	37.3	248	S55066	tissue kallikrein
6	509	37.2	261	1 NGMSG	7S nerve growth fa
7	507	37.0	261	A34079	tissue kallikrein
8	506	37.0	247	A27547	trypsin (EC 3.4.21
9	506	37.0	261	S01971	tissue kallikrein
10	503	36.7	261	JE0236	tissue kallikrein
11	503	36.7	261	A11136	tissue kallikrein
12	502.5	36.7	246	JQ1472	trypsin (EC 3.4.21
13	502.5	36.7	261	A29586	tissue kallikrein
14	502	36.7	261	A41020	tissue kallikrein
15	501.5	36.6	250	T01779	trypsin (EC 3.4.21
16	499.5	36.5	246	1 TRDC	trypsin (EC 3.4.21
17	498	36.4	261	A32297	semenogelase (EC 3
18	497	36.3	247	S05494	trypsin (EC 3.4.21
19	497	36.3	259	B31136	tissue kallikrein
20	496	36.2	248	S55067	trypsin (EC 3.4.21
21	496	36.2	259	A29746	tissue kallikrein
22	496	36.2	265	1 KQRTP	tissue kallikrein
23	495.5	36.2	246	JQ1471	trypsin (EC 3.4.21
24	492.5	36.0	261	A29745	tissue kallikrein
25	492	35.9	257	S33772	tissue kallikrein
26	491	35.9	261	1 EGMSB	tissue kallikrein
27	488.5	35.7	261	A25606	tissue kallikrein
28	487.5	35.6	262	1 KQHU	tissue kallikrein
29	485	35.4	246	1 TRRT1	trypsin (EC 3.4.21

30	485	35.4	261	1 S35711	semenogelase (EC 3
31	484	35.4	259	1 KORTTW	tonin (EC 3.4.21.-
32	484	35.4	261	1 TRMSM5	tissue kallikrein
33	480	35.1	247	2 S13813	trypsin (EC 3.4.21
34	480	35.1	261	1 KQMS1	tissue kallikrein
35	479.5	35.0	249	1 TRBOTR	trypsin (EC 3.4.21
36	479	35.0	226	2 B25528	trypsin (EC 3.4.21
37	476.5	34.8	242	2 S49489	trypsin (EC 3.4.21
38	472.5	34.5	231	1 TRPGTR	trypsin (EC 3.4.21
39	472.5	34.5	247	1 TRDG	trypsin (EC 3.4.21
40	471	34.4	259	2 D23863	tissue kallikrein
41	470.5	34.4	263	2 S15686	tissue kallikrein
42	470	34.3	243	2 A35871	trypsin (EC 3.4.21
43	469.5	34.3	260	2 A37938	tissue kallikrein
44	467.5	34.1	238	2 S31779	trypsin (EC 3.4.21
45	467.5	34.1	247	1 A25852	trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE - precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A53968
R:Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A:Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzy
M:Reference number: A53968; MUID:94308225; PMID:8034709
A:Accession: A53968
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <HAN>
A:Cross-references: UNIPROT:P49862; GB:I33404; NID:9521214; PIDN:AAC37551.1; PID:953250
C:Genetics:
A:Gene: GDB:PRSS6; SCCE
A:Map position: 7q35-7q35
A:Superfamily: trypsin; trypsin homology
F:30-245/Domain: trypsin homology <TRY>

Query Match	41.5%;	Score	567.5;	DB 2;	Length	253;			
Best Local Similarity	46.2%;	Pred. No.	1.7e-41;						
Matches	111;	Conservative	40;	Mismatches	82;	Indels	7;	Gaps	4;
y	15	LILGVAGSLVSGSCQIINGEDCSPHSQPWQALVWELFSGVIVHPQWVLSAAHCQ	74						
b	16	LAETAGEAQG--DKIIDGAPCARGSHPWQVALLSGNLHCGVILWNERVLTAAHCKM	73						
y	75	NSYITGLHLSLEADQEPGSCQMVESLSVRHPEYRPLLANDMLIKLDESSESDETIRS	134						
b	74	NEYTVHLGSDTL-GDRL--AQRIKASKSRHPGYSQTQTHVNDMLVKLNSQARLSMWVK	130						
y	135	ISIASQCPTAGNSCLVSGHGLIANG--RMPTVLQCVNVSVEEVCCKSLYDLYPHSMFC	192						
b	131	VLPRLSRCEPPGTCTVSGNGTTTSPDVTFFPSDLMCDVDVKLISPDQCTKYVKDLLENMLC	190						
y	193	AGGGQDQKDCNCGDGGPLICNGYLGVLGFKAPCGQVGVGVYTNLCRFTWIEKTVQ	252						
b	191	AGIPDSKKACNCGDGGPLVCRGTLLQGLVSWGTFPCGQPNDRPVYTVQVCKFTKWINDMK	250						

RESULT 2

I56559
neuropsin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishi
J. Neurosci. 15, 5088-5097, 1995

A>Title: Expression and activity-dependent changes of a novel limbic-serine protease gene
A/Reference number: I56559; MUID:95348817; PMID:7623137

A/Accession: I56559

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-260 <RES>

A/Cross-references: UNIPROT:061955; GB:D30785; NID:g1648847; PIDN:BA06451.1; PID:g10200

C:Superfamily: trypsin; trypsin homology

F:33-252/Domain: trypsin homology <TRY>

Query Match 41.2%; Score 563.5; DB 2; Length 260;
Best Local Similarity 41.3%; Pred. No. 3.8e-41;
Matches 102; Conservative 47; Mismatches 91; Indels 7; Gaps 4;

QY 10 WFLGVLILVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCGVLVHPQWLISA 69

DB 12 WLLLLFWAGAGLTRAQSKILEGECIPHSQPWQAALFQGERLICGVLVGDRLVITA 71

QY 70 AHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYNRPL---LANDMLIKLDESIV 126

DB 72 AHCKKQKYSVRLGDRSLQSDQP-EQEIQAQSIQHPCVYNSNPEDSHDMLIRLQNSA 130

QY 127 SSSDTRISISASQCTAGNSCLVSGWGLLANGR--MPTVLCQVNVSVSEVCSKLIDP 184

DB 131 NLGDKVKPQLANLCPKVGKQCIISGSGFTVSPQENFTNLCAEVKIYSQNKCEAYPG 190

QY 185 LVHPSMFACAGGQDQKDSGNSGSGPLICNGYLOGLVSGKAPCGQGVGPGVYTNLCRFT 244

DB 191 KITEGMVCA-GSSNGADTCQDSGGFLVCDGMLQGITWSGSDPCPKPEKPGVYTKICRYT 249

QY 245 EWIEKTV 251

DB 250 TWIKKT 256

RESULT 3

S45303

tissue kallikrein (EC 3.4.21.35) precursor - dog

C:Species: Canis lupus familiaris (dog)

C/Date: 20-Oct-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C/Accession: S45303; 938487

R/Gauthier, E.R.; Dumas, C.; Chadelain, P.; Tremblay, R.R.; Dube, J.Y.

Biochim. Biophys. Acta 1218, 102-104, 1994

A>Title: Characterization of canine pancreas kallikrein cDNA.

A/Reference number: S45303; MUID:94250683; PMID:8193155

A/Accession: S45303

A/Molecule type: mRNA

A/Residues: 1-261 <GAU>

A/Cross-references: UNIPROT:Q29474; EMBL:X75479; NID:g414018; PIDN:CAA53210.1; PID:g4140

C:Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; serine proteinase

F:1-24/Domain: signal sequence

F:25-261/Product: tissue kallikrein #status predicted <SIG>

F:25-253/Domain: trypsin homology <TRY>

F:165,120,213/Active site: His, Asp, Ser #status predicted

Query Match 38.3%; Score 524; DB 2; Length 261;

Best Local Similarity 40.3%; Pred. No. 9.7e-38;

Matches 106; Conservative 51; Mismatches 84; Indels 22; Gaps 6;

QY 10 WFLGY-LILVAGSLVSGSC-----SQIINGEDCSPHSQPQWQAALVMENELFCGVLVHPQ 64

DB 2 WFLVCLALSLAG---TGAAPVPVSRITGGWDCTKNSQPWQAALVHYSKFCGGLVHPPE 58

QY 65 WVLSSAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYNRPLAN-----115

DB 59 WVVTAACHINDNYQLWGLRYNL-FHEHTAQPVQVRESFPFPEFNLKHLKHLRPLEEDY 117

QY 116 --DMLIKLDESVSSEDTIRISISASQCTAGNSCLVSGWGLLANGRM--PTVLCQVNV 171

DB 118 SHDMLRLAEPQAQITDAVRVLDLTQFPQVSGTCSYAGWSGSIKPKFIYPDDLCQVDLE 177

QY 172 VVSEVCSKLVDPLVHPSMFCAGGQDQKDSGNSGSGPLICNGYLOGLVSGKAPCGQV 231

DB 178 LLSNDICANAHSQKVTPEMLCAGHLEGCKDTGSDGGFLICDGVLOGITSGHVGPCGSP 237

QY 232 GVPGVYTNLCRFTETWIEKTVQAS 254

DB 238 NMPAVYTKVISHLEWIKETMTAN 260

RESULT 4

A44284

tissue kallikrein (EC 3.4.21.35) homolog - rat (fragment)

N/Alternate names: proteinase B light chain

C:Species: Rattus norvegicus (Norway rat)

C/Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A44284; C41429

R/Ma, J.X.; Chao, J.; Chao, L.

Biochemistry 31, 10922-10928, 1992

A>Title: Molecular cloning and characterization of rKlk10, a cDNA encoding T-kininogenas

A/Reference number: A44284; MUID:93041794; PMID:1420203

A/Accession: A44284

A>Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-244 <MAL>

A/Cross-references: UNIPROT:P36375; GB:S48142; NID:g259430; PIDN:AAB24071.1; PID:g259434

A/Experimental source: submandibular gland

A/Note: sequence extracted from NCBI backbone (NCBIN:118095, NCBI:P:118096)

R/Kato, H.; Nakanishi, E.; Enjiyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.

J. Biochem. 102, 1389-1404, 1987

A>Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi

A/Reference number: A41429; MUID:88198057; PMID:3482210

A/Accession: C41429

A>Status: preliminary

A/Molecule type: protein

A/Residues: 10-61 <KAT>

C:Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; serine proteinase

F:10-236/Domain: trypsin homology <TRY>

F:48,103,196/Active site: His, Asp, Ser #status predicted

Query Match 37.6%; Score 515; DB 2; Length 244;

Best Local Similarity 42.4%; Pred. No. 5.3e-37;

Matches 101; Conservative 42; Mismatches 77; Indels 18; Gaps 5;

QY 29 SQIINGEDCSPHSQPQWQAALVMENELFCGVLVHPQWLSAAHCFQNSYITIGLHLSLEA 88

DB 8 SRIVGVYKCKNSQPVQVAII--NEYLGGVLIDPSWVITAAHCYSNYHYHLLGRNNLFE 65

QY 89 DQEPGQSMVEASLSVRHPEYNRPL-----ANDMLIKLDESVSSEDTIRIS 136

DB 66 D-EPPAQVRFVNSQSPFHPDY-KPFLMRNHTRQRGDYSNDLMLLHLSBPADITDGVKVID 123

QY 137 IASQCPAGNSCLVSGWGLL--ANGRMPTVLCQVNVSVSEVCSKLIDPLVHPSMFCAG 194

DB 124 LPTBEPKVGSTCLASGWSGSKPLNWEIPDDIQCQVNIHLHLSNEKCIETAEYEQKVTDLMLCAG 183

QY 195 GGQDQKDSGNSGSGPLICNGYLOGLVSGKAPCGQGVGPGVYTNLCRFTETWIEKTVQ 252

DB 184 EMDGRKTCRKGDSGGPLICDGVLOGITSGHVGPCGSP 241

RESULT 5

S55066

trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken

N/Alternate names: trypsinogen II

C:Species: Gallus gallus (chicken)

C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C/Accession: S55066; S72347

R/Wang, K.; Gan, L.; Lee, I.; Hood, L.

Biochem. J. 307, 471-479, 1995

A>Title: Isolation and characterization of the chicken trypsinogen gene family.

A/Reference number: S55065; MUID:95251611; PMID:7733885

A/Accession: S55066

A/Molecule type: mRNA

J. Biol. Chem. 256, 9156-9166, 1981

A;Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S n

A;Reference number: A92341; MUID:81264363; PMID:7263706

A;Accession: A92341

A:Molecule type: protein

A;Residues: 25-107,112-261 <THO>

A;Experimental source: outbred strain Swiss Webster

C;Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer compose

C;Comment: The active form of the gamma chain occurs naturally as combinations of eithe

C;Genetics:

A;Map position: 7

A;Introns: 16/1; 69/2; 165/1; 210/3

C;Superfamily: trypsin; trypsin homology

C;Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gl

F;1-18/Domain: signal sequence #status predicted <SIG>

F;25-253/Domain: trypsin homology <TRY>

E;25-107/Domain: segment B1 <GB1>

E;25-107,112-261/Product: nerve growth factor gamma chain (active form) #status experim

F;112-261/Domain: segment A <GAA>

F;112-164/Domain: segment C <GCC>

F;165-261/Domain: segment B2 <GB2>

F;31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted

E;65,120,213/Active site: His, Asp, Ser #status predicted

F;102/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 37.2%; Score 509; DB 1; Length 261;
Best Local Similarity 39.5%; Pred. No. 1.9e-36;
Matches 103; Conservative 48; Mismatches 86; Indels 24; Gaps 6;

Qy 10 WFL-GYLLGVAG-SLVSGSCQINGEDCSPHSQPQAALVMENELFCSGVLVHPQWVL 67
 ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 2 WFLILFALSGLGIDAAPPVQSRIIVGFGRKCKNSQPWHVAIYRYTQLCGGVLLDPNWVL 61
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 68 SAACHCFQNSYTIGLGHLSLEADQPGCSQMVVEASISVYRHPENVRL-----AND 116
 :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 62 TAAHCYDDNYKVMLGKNUNLFKD-EPSAQHRFVSKAIPHGFNMSLMRKHIRFLEYDYSND 120
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 117 LMLIKLDSESVSDTRISITSIASQCPTAGNSCLVSGMGLLANGRMPTVLQ-----CVNV 170
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 121 LMLLRSLKPADITDVKPIITLTERPKLSTCLASGWSIT----PYKFQFTDDLVCYNL 176
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 171 SVSBEVCSKULYDIYPHSFMFCAGGQQDKDSNCNGSGGPLICNGYIQGLVSFGKAPCQG 230
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 177 KLLPNEDCAKAHIEKVTDAMLKAGEMDGKGDTCKGDSGGPLICDGLVIGITSWGHTPCGE 236
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 231 VGPVGVTNLCKFTIEWIEKTIV 251
 :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 237 PDMPGVVTKLNKFTSWIKDTM 257
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 7

A34079

tissue kallikrein (EC 3.4.21.35) P1 precursor - rat

N;Alternate names: kallikrein-related proteinase k8

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004

C;Accession: A34079; S10700

E;Brady, J.M.; Wines, D.R.; MacDonald, R.J.

Biochemistry 28, 5203-5210, 1989

A;Title: Expression of two kallikrein gene family members in the rat prostate.

A;Reference number: A34079; MUID:89352606; PMID:2765531

A;Accession: A34079

A>Status: preliminary

A:Molecule type: DNA; mRNA

A;Residues: 1-261 <BRA>

A;Cross-references: UNIPROT:P36374; GB:M27215; GB:M27216; GB:M27217; NID:g206638; PRDN:

A;Experimental source: prostate

R:Eumoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.

FEBS Lett. 265, 137-140, 1990

A;Title: Substrate specificity of two kallikrein family gene products isolated from the

A;Reference number: S10698; MUID:90306305; PMID:2194829

A;Accession: S10700

A:Molecule type: protein

A:Molecule type: mRNA
A:Residues: 1-250 <LEA>
A:Cross-references: EMBL:X56744; NID:g1213630; PID:g64240
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F:23-242/Domain: trypsin homology <TRY>

Query Match 36.6%; Score 501.5; DB 2; Length 250;
Best Local Similarity 42.3%; Pred. No. 8e-36;
Matches 105; Conservative 37; Mismatches 97; Indels 9; Gaps 5;

QY	12	LGVLILGVAGSLVSGSQIINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAH	71
DB	4	LALLLVGAAVAVPREDEGRIIGHECAHSRPFMASLNYGYH-FCGGVLINQWVLSVAH	62
QY	72	CFQNSYT--IGLGLHSLQADQEPGQWVEASLSVRHPEYNRPRLANDLMLIKLDESVSSES	129
DB	63	CWYNPVAMQVMLGEHDLR-KFEGTEQLMKTTDTIWHPNVDYQTLDFDIMLIKLYHPVEVS	121
QY	130	DTIRISISIASQCPTAGNSCLVSGWLLANG----RMPTVLQCVNVSVSEVCSKLYDPL	185
DB	122	HAVGPIPLPTSCPVAGTPCSVSGWNTARDGDEVYLTLLQCMDFIVDDEEQCMKSYDPM	181
QY	186	YHPSMFCAGGQDQKDSNGDSGGPLICNGYLOGLYSFGKAPCGGVGVGVVYTNLCKFTE	245
DB	182	ISPRMVCAGFMGDSRDACNGDSGLVCRGEVYGLVSWGQG-CAQPNYPGVVYVYKLCFLG	240
QY	246	WIEKTVQA	253
DB	241	WIEKTVQA	248

Search completed: February 10, 2005, 08:55:01
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:54:22 ; Search time 128 Seconds
(without alignments)
648.393 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPMGWFGLYLGLVA.....GVYTNLCRFTWIEKTVQAS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1369	100.0	254	9 US-09-759-143-525	Sequence 525, App
2	1369	100.0	254	9 US-09-780-669-525	Sequence 525, App
3	1369	100.0	254	9 US-09-822-827-525	Sequence 525, App
4	1369	100.0	254	9 US-09-895-793-525	Sequence 525, App
5	1369	100.0	254	9 US-09-895-814-525	Sequence 525, App
6	1369	100.0	254	13 US-10-012-896-525	Sequence 525, App
7	1369	100.0	254	14 US-10-010-940-525	Sequence 525, App
8	1369	100.0	254	14 US-10-144-678A-525	Sequence 525, App
9	1369	100.0	254	14 US-10-294-025-525	Sequence 525, App
10	1369	100.0	254	16 US-10-473-485-6	Sequence 6, Appli
11	1369	100.0	254	16 US-10-473-485-13	Sequence 13, Appli
12	1369	100.0	1079	9 US-09-822-827-947	Sequence 947, App
13	1369	100.0	1079	9 US-09-895-793-947	Sequence 947, App

14	1364	99.6	254	14	US-10-312-089-7	Sequence 7, Appli
15	1352	98.8	254	9	US-09-759-143-523	Sequence 523, App
16	1352	98.8	254	9	US-09-780-669-523	Sequence 523, App
17	1352	98.8	254	9	US-09-822-827-523	Sequence 523, App
18	1352	98.8	254	9	US-09-895-793-523	Sequence 523, App
19	1352	98.8	254	9	US-09-895-814-523	Sequence 523, App
20	1352	98.8	254	13	US-10-012-896-523	Sequence 523, App
21	1352	98.8	254	14	US-10-010-940-523	Sequence 523, App
22	1352	98.8	254	14	US-10-144-678A-523	Sequence 523, App
23	1352	98.8	254	14	US-10-294-025-523	Sequence 523, App
24	1348.5	98.5	253	15	US-10-344-334-37	Sequence 37, Appli
25	1205	88.0	449	9	US-09-759-143-617	Sequence 617, App
26	1205	88.0	449	9	US-09-780-669-617	Sequence 617, App
27	1205	88.0	449	9	US-09-822-827-617	Sequence 617, App
28	1205	88.0	449	9	US-09-895-793-617	Sequence 617, App
29	1205	88.0	449	9	US-09-895-814-617	Sequence 617, App
30	1205	88.0	449	13	US-10-012-896-617	Sequence 617, App
31	1205	88.0	449	14	US-10-144-678A-617	Sequence 617, App
32	1205	88.0	449	14	US-10-294-025-617	Sequence 617, App
33	1205	88.0	585	9	US-09-822-827-978	Sequence 978, App
34	1205	88.0	585	9	US-09-822-827-981	Sequence 981, App
35	1205	88.0	585	9	US-09-895-793-978	Sequence 978, App
36	1205	88.0	585	9	US-09-895-793-981	Sequence 981, App
37	1205	88.0	585	14	US-10-144-678A-1020	Sequence 1020, Ap
38	1205	88.0	585	14	US-10-294-025-1020	Sequence 1020, Ap
39	1205	88.0	801	9	US-09-822-827-982	Sequence 982, App
40	1205	88.0	801	9	US-09-895-793-982	Sequence 982, App
41	1191	87.0	226	14	US-10-312-089-8	Sequence 8, Appli
42	1191	87.0	312	14	US-10-312-089-3	Sequence 3, Appli
43	1191	87.0	344	9	US-09-822-827-973	Sequence 973, App
44	1191	87.0	344	9	US-09-895-793-973	Sequence 973, App
45	1185	86.6	220	9	US-09-759-143-327	Sequence 327, App

ALIGNMENTS

RESULT 1
US-09-759-143-525
; Sequence 525, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-525
Query Match 100.0%; Score 1369; DB 9; Length 254;

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Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
QY 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPNMFCAAGGQDQKDCSNGDSGGPLICNGYLQGLVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPNMFCAAGGQDQKDCSNGDSGGPLICNGYLQGLVSFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 2
US-09-780-669-525
; Sequence 525, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
QY 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPNMFCAAGGQDQKDCSNGDSGGPLICNGYLQGLVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPNMFCAAGGQDQKDCSNGDSGGPLICNGYLQGLVSFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 3
US-09-822-827-525
; Sequence 525, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
QY 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPNMFCAAGGQDQKDCSNGDSGGPLICNGYLQGLVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPNMFCAAGGQDQKDCSNGDSGGPLICNGYLQGLVSFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 4
US-09-895-793-525
; Sequence 525, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
```

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; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-525

Query Match      100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
DB      1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60

QY      61 VHPQWLSAAHCFQNSYTTIGLGLHSLAQDEPGSQMVEASLSVRHPEYNRPILLANDMLI 120
DB      61 VHPQWLSAAHCFQNSYTTIGLGLHSLAQDEPGSQMVEASLSVRHPEYNRPILLANDMLI 120

QY      121 KLDESVSSEDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB      121 KLDESVSSEDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY      181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
DB      181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240

QY      241 CKFTWIEKTVQAS 254
DB      241 CKFTWIEKTVQAS 254

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RESULT 5

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US-09-895-814-525
; Sequence 525, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Xuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```

```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-525

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Query Match      100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
DB      1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60

QY      61 VHPQWLSAAHCFQNSYTTIGLGLHSLAQDEPGSQMVEASLSVRHPEYNRPILLANDMLI 120
DB      61 VHPQWLSAAHCFQNSYTTIGLGLHSLAQDEPGSQMVEASLSVRHPEYNRPILLANDMLI 120

QY      121 KLDESVSSEDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB      121 KLDESVSSEDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY      181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
DB      181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240

QY      241 CKFTWIEKTVQAS 254
DB      241 CKFTWIEKTVQAS 254

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RESULT 6

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US-10-012-896-525
; Sequence 525, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Xuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-525

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; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-525

Query Match      100.0%; Score 1369; DB 13; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVWNEELFCSGVL 60
Db 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVWNEELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120
Db 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120

QY 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180
Db 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180

QY 181 LYDPLYPHMFCAAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHMFCAAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240

QY 241 CKFTEWIEKTVOAS 254
Db 241 CKFTEWIEKTVOAS 254

RESULT 8
US-10-144-678A-525
; Sequence 525, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-525

Query Match      100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVWNEELFCSGVL 60
Db 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVWNEELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120
Db 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120

QY 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180
Db 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180

QY 181 LYDPLYPHMFCAAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHMFCAAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240

QY 241 CKFTEWIEKTVOAS 254
Db 241 CKFTEWIEKTVOAS 254

RESULT 7
US-10-010-940-525
; Sequence 525, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-525

Query Match      100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVWNEELFCSGVL 60
Db 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVWNEELFCSGVL 60
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Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254

RESULT 9

US-10-294-025-525
; Sequence 525, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-525

Query Match 100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Qy 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254

RESULT 10

US-10-473-485-6
; Sequence 6, Application US/10473485
; Publication No. US20040137455A1
; GENERAL INFORMATION:
; APPLICANT: Clements, Judith A.
; APPLICANT: Dong, Ying
; TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign
; FILE REFERENCE: DAV1172.004APC
; CURRENT APPLICATION NUMBER: US/10/473,485
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: AU PR4022/01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6

; LENGTH: 254
; TYPE: PRT
; ORGANISM: human
US-10-473-485-6
Query Match 100.0%; Score 1369; DB 16; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Qy 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254

RESULT 11

US-10-473-485-13
; Sequence 13, Application US/10473485
; Publication No. US20040137455A1
; GENERAL INFORMATION:
; APPLICANT: Clements, Judith A.
; APPLICANT: Dong, Ying
; TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign
; FILE REFERENCE: DAV1172.004APC
; CURRENT APPLICATION NUMBER: US/10/473,485
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: AU PR4022/01
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 254
; TYPE: PRT
; ORGANISM: human
US-10-473-485-13

Query Match 100.0%; Score 1369; DB 16; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Qy 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLANGMPVTLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDSNGSDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254

Db 241 CKTEWIEKTVOAS 254

RESULT 12

US-09-822-827-947

; Sequence 947, Application US/09822827

; Patent No. US20020081680A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827

; PRIORITY FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 947

; LENGTH: 1079

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-822-827-947

Query Match 100.0%; Score 1369; DB 9; Length 1079;

Best Local Similarity 100.0%; Pred. No. 8.4e-129;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60

Db 271 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 330

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 120

Db 331 VHPQWLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 390

QY 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

Db 391 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 450

QY 181 LYDPLVHPMFAGGQDQKSCNDSGGPLICNGYLOGLVFGKAPCGQGVPGVYTNL 240

Db 451 LYDPLVHPMFAGGQDQKSCNDSGGPLICNGYLOGLVFGKAPCGQGVPGVYTNL 510

QY 241 CKTEWIEKTVOAS 254

Db 511 CKTEWIEKTVOAS 524

RESULT 13

US-09-895-793-947

; Sequence 947, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C2

; CURRENT APPLICATION NUMBER: US/09/895,793

; PRIORITY FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 947

; LENGTH: 1079

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-793-947

Query Match 100.0%; Score 1369; DB 9; Length 1079;

Best Local Similarity 100.0%; Pred. No. 8.4e-129;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60

Db 271 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 330

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 120

Db 331 VHPQWLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 390

QY 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

Db 391 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 450

QY 181 LYDPLVHPMFAGGQDQKSCNDSGGPLICNGYLOGLVFGKAPCGQGVPGVYTNL 240

Db 451 LYDPLVHPMFAGGQDQKSCNDSGGPLICNGYLOGLVFGKAPCGQGVPGVYTNL 510

QY 241 CKTEWIEKTVOAS 254

Db 511 CKTEWIEKTVOAS 524

RESULT 14

US-10-312-089-7

; Sequence 7, Application US/10312089

; Publication No. US20030143240A1

; GENERAL INFORMATION:

; APPLICANT: Cabezon-Silva, Teresa Elisa Virginia

; APPLICANT: Permann, Philippe Jean Gervais Ghislain

; TITLE OF INVENTION: Prostate Protein Vaccine Comprising

; TITLE OF INVENTION: Derivatized Thiol Residues and Methods for Producing Said

; TITLE OF INVENTION: Antigen

; FILE REFERENCE: B45224

; CURRENT APPLICATION NUMBER: US/10/312,089

; PRIORITY FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: PCT/EP01/07082

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: GB 0015722.2

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-312-089-7

Query Match 99.6%; Score 1364; DB 14; Length 254;

Best Local Similarity 99.6%; Pred. No. 4.1e-129;

Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60

Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 120

Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
QY 181 LYDPLYPHSMFPCAGGQDQKDSNCGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFPCAGGQDQKDSNCGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 15

US-09-759-143-523
; Sequence 523, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-759-143-523

Query Match 98.8%; Score 1352; DB 9; Length 254;
Best Local Similarity 98.8%; Pred. No. 6.7e-128;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
Db 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
QY 181 LYDPLYPHSMFPCAGGQDQKDSNCGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240

Db 181 LYDPLYPHSMFPCAGGQXQXDSNCGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254
Search completed: February 10, 2005, 09:06:41
Job time : 129 secs

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Db 241 CKFTWIEKTVQAS 254
|||||
RESULT 2
US-09-636-215-525
; Sequence 525, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLLANDMLI 120
|
Db 61 VHPQWVLSAAHCFQNSYTTIGLGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLLANDMLI 120
|
QY 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
Db 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
Db 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
QY 241 CKFTWIEKTVQAS 254
|
Db 241 CKFTWIEKTVQAS 254
|

RESULT 3
US-09-685-166A-525
; Sequence 525, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLLANDMLI 120
|
Db 61 VHPQWVLSAAHCFQNSYTTIGLGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLLANDMLI 120
|
QY 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
Db 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
Db 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
QY 241 CKFTWIEKTVQAS 254
|
Db 241 CKFTWIEKTVQAS 254
|

RESULT 4
US-09-679-426-525
; Sequence 525, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
```

```
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-685-166A-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLLANDMLI 120
|
Db 61 VHPQWVLSAAHCFQNSYTTIGLGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLLANDMLI 120
|
QY 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
Db 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
Db 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
QY 241 CKFTWIEKTVQAS 254
|
Db 241 CKFTWIEKTVQAS 254
|

RESULT 4
US-09-679-426-525
; Sequence 525, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
```

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE REFERENCE: 210121.427C20
;; CURRENT APPLICATION NUMBER: US/09/679,426
;; CURRENT FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 895
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 525
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-679-426-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLVHPMFAGGQDQKSCNGSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
DB 181 LYDPLVHPMFAGGQDQKSCNGSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 5

US-09-759-143-525
; Sequence 525, Application US/09759143
; Patent No. 6800746

GENERAL INFORMATION:

;; APPLICANT: Xu, Jiangchun
;; APPLICANT: Dillon, Davin C.
;; APPLICANT: Mitcham, Jennifer L.
;; APPLICANT: Harlocker, Susan L.
;; APPLICANT: Jiang, Yuqui
;; APPLICANT: Henderson, Robert A.
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Retter, Marc W.
;; APPLICANT: Stolk, John A.
;; APPLICANT: Day, Craig H.
;; APPLICANT: Vedvick, Thomas S.
;; APPLICANT: Carter, Darrick
;; APPLICANT: Li, Samuel
;; APPLICANT: Wang, Aijun
;; APPLICANT: Skeiky, Yasir A.W.

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE REFERENCE: 210121.427C23

;; CURRENT APPLICATION NUMBER: US/09/759,143
;; CURRENT FILING DATE: 2001-01-12
;; NUMBER OF SEQ ID NOS: 934
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 525

;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapien

US-09-759-143-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLVHPMFAGGQDQKSCNGSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
DB 181 LYDPLVHPMFAGGQDQKSCNGSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 6

US-09-651-236-525
; Sequence 525, Application US/09651236
; Patent No. 6818751

GENERAL INFORMATION:

;; APPLICANT: Xu, Jiangchun
;; APPLICANT: Dillon, Davin C.
;; APPLICANT: Mitcham, Jennifer L.
;; APPLICANT: Harlocker, Susan L.
;; APPLICANT: Jiang, Yuqui
;; APPLICANT: Henderson, Robert A.
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Retter, Marc W.
;; APPLICANT: Stolk, John A.
;; APPLICANT: Day, Craig H.
;; APPLICANT: Vedvick, Thomas S.
;; APPLICANT: Carter, Darrick
;; APPLICANT: Li, Samuel
;; APPLICANT: Wang, Aijun
;; APPLICANT: Skeiky, Yasir A.W.

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE REFERENCE: 210121.42718C18

;; CURRENT APPLICATION NUMBER: US/09/651,236
;; CURRENT FILING DATE: 2000-08-29
;; NUMBER OF SEQ ID NOS: 865
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 525

;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapien

US-09-651-236-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

Db 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPMFACAGGQDQKDCNCGSGGGLICNGYLGVLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLVHPMFACAGGQDQKDCNCGSGGGLICNGYLGVLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 7

US-09-439-313-523

; Sequence 523, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqui

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 523

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

; NAME/KEY: VARIANT

; LOCATION: (1)...(254)

; OTHER INFORMATION: Xaa = Any amino acid

US-09-439-313-523

Query Match 98.8%; Score 1352; DB 3; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLSAHCQFQNSYTTIGLHLSLEADQEPGQMVESASLSVRHPEYNRPFLANDLMLI 120
Db 61 VHPQWLSAHCQFQNSYTTIGLHLSLEADQEPGQMVESASLSVRHPEYNRPFLANDLMLI 120
QY 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPMFACAGGQDQKDCNCGSGGGLICNGYLGVLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLVHPMFACAGGQDQKDCNCGSGGGLICNGYLGVLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 8

US-09-636-215-523

; Sequence 523, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, William
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-636-215-523

Query Match 98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLSAHCQFQNSYTTIGLHLSLEADQEPGQMVESASLSVRHPEYNRPFLANDLMLI 120
Db 61 VHPQWLSAHCQFQNSYTTIGLHLSLEADQEPGQMVESASLSVRHPEYNRPFLANDLMLI 120
QY 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPMFACAGGQDQKDCNCGSGGGLICNGYLGVLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLVHPMFACAGGQDQKDCNCGSGGGLICNGYLGVLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 9

US-09-685-166A-523

; Sequence 523, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

```
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-685-166A-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLEADQEPGSMQVEASLSVRHPEYNRPLLANDLMLI 120
DB 61 VHPQWLSATHCFQNSYTTIGLGLHSLEADQEPGSMQVEASLSVRHPEYNRPLLANDLMLI 120

QY 121 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLVHPSMFCAGGGQXQXDS CNGSDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240
DB 181 LYDPLVHPSMFCAGGGQXQXDS CNGSDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 10
US-09-679-426-523
; Sequence 523, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jjiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
```

```
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-679-426-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLEADQEPGSMQVEASLSVRHPEYNRPLLANDLMLI 120
DB 61 VHPQWLSATHCFQNSYTTIGLGLHSLEADQEPGSMQVEASLSVRHPEYNRPLLANDLMLI 120

QY 121 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLVHPSMFCAGGGQXQXDS CNGSDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240
DB 181 LYDPLVHPSMFCAGGGQXQXDS CNGSDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 11
US-09-759-143-523
; Sequence 523, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jjiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
```

; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-759-143-523

Query Match 98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
Db 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLVAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Db 61 VHPQWLVAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
QY 121 KLDSESVESDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQXQXDSGNGDGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
Db 181 LYDPLYPHSMFCAGGQXQXDSGNGDGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
QY 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254

RESULT 12

US-09-651-236-523
; Sequence 523, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-651-236-523

Query Match 98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
Db 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLVAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Db 61 VHPQWLVAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
QY 121 KLDSESVESDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQXQXDSGNGDGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
Db 181 LYDPLYPHSMFCAGGQXQXDSGNGDGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
QY 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254

RESULT 13

US-09-636-215-617
; Sequence 617, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 617
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.3e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQ 90
Db 8 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQ 67

QY 91 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRISIASQCPTAGNSCLV 150
Db 68 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRISIASQCPTAGNSCLV 127
QY 151 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 210
Db 128 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 187
QY 211 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS 254
Db 188 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS 231

RESULT 14

US-09-685-166A-617
; Sequence 617, Application US/09685166A
; Patent No. 6630305

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 617
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-685-166A-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.3e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 90
Db 8 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 67
QY 91 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRISIASQCPTAGNSCLV 150
Db 68 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRISIASQCPTAGNSCLV 127
QY 151 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 210
Db 128 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 187
QY 211 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS 254
Db 188 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS 231

RESULT 15

US-09-679-426-617
; Sequence 617, Application US/09679426

; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 617
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-679-426-617

Query Match 88.0%; Score 1205; DB 4; Length 449;

Best Local Similarity 100.0%; Pred. No. 4.3e-115;

Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 90
Db 8 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 67
QY 91 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRISIASQCPTAGNSCLV 150
Db 68 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRISIASQCPTAGNSCLV 127
QY 151 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 210
Db 128 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 187
QY 211 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS 254
Db 188 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS 231

Search completed: February 10, 2005, 08:55:49

Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:36:55 ; Search time 166 Seconds
 (without alignments)
 591.790 Million cell updates/sec

Title: US-09-895-814-525
 Perfect score: 1369
 Sequence: 1 MATAGNPGWFLGYLILGVA.....GVYTNLCKFTWEIKTVQAS 254

Scoring table: BLASTUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseq19808:*
 - 2: Geneseq19908:*
 - 3: Geneseq20008:*
 - 4: Geneseq20018:*
 - 5: Geneseq20028:*
 - 6: Geneseq20038:*
 - 7: Geneseq20038s:*
 - 8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1369	100.0	254	3 AAB21294	Aab21294 Human KLK
2	1369	100.0	254	4 AAM01174	Aam01174 Human pro
3	1369	100.0	254	4 AAU69819	Aau69819 Human pro
4	1369	100.0	254	4 AAG99059	Aag99059 Human pro
5	1369	100.0	254	4 ABU71710	Abu71710 Prostate
6	1369	100.0	254	5 ABB95279	Abb95279 Human P70
7	1369	100.0	254	6 ABP54360	Abp54360 Human KLK
8	1369	100.0	254	6 ABP54357	Abp54357 Human KLK
9	1369	100.0	254	6 ABR54391	AbR54391 Prostate
10	1369	100.0	254	7 ADB13975	Adb13975 Human pro
11	1369	100.0	254	7 ADG26391	Adg26391 Human pro
12	1369	100.0	1079	4 AAB74830	Aab74830 Prostate
13	1369	100.0	1079	4 ABU71860	Abu71860 Prostate
14	1364	99.6	254	3 AAB21320	Aab21320 Human pro
15	1364	99.6	254	4 AAV72525	Aav72525 Human pro
16	1364	99.6	254	5 AAU74901	Aau74901 Protein s
17	1364	99.6	254	5 AAU74932	Aau74932 Amino aci
18	1352	98.8	254	4 AAM01173	Aam01173 Human pro
19	1352	98.8	254	4 AAU69818	Aau69818 Human pro
20	1352	98.8	254	4 AAG99058	Aag99058 Human pro
21	1352	98.8	254	4 AAB71709	Abu71709 Prostate
22	1352	98.8	254	5 ABB95278	Abb95278 Human P70
23	1352	98.8	254	6 ABR54390	AbR54390 Prostate
24	1352	98.8	254	7 ADB13973	Adb13973 Human mat
25	1352	98.8	254	7 ADG26389	Adg26389 Human pro

RESULT 1
 AAB21294
 ID AAB21294 standard; protein; 254 AA.
 XX AAB21294;
 AC AAB21294;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human KLK-L1 protein #2.
 XX
 KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
 KW kallikrein-like protein; serine protease; cytosolic; cancer;
 KW prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2000053776-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-CA000258.
 XX
 PR 11-MAR-1999; 99US-0124260P.
 PR 01-APR-1999; 99US-0127386P.
 PR 21-JUL-1999; 99US-0144919P.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 XX
 PI Yousef GM, Diamandis EP;
 XX
 WPI; 2000-587440/55.
 DR N-PSDB; AAA95896.
 XX
 PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
 protein mediated disorders, especially cancer.
 XX
 Claim 8; Page 141; 184pp; English.
 CC The present sequence is kallikrein-like protein KLK-L1. Kallikreins and
 CC kallikrein-like proteins are a subgroup of the serine protease enzyme
 CC family. They catalyse the selective cleavage of specific polypeptide
 CC precursors to release peptides with potent biological activity. Nucleic
 CC acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
 CC KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
 CC treatment, monitoring and diagnosis of cancers, especially prostate
 CC cancer. They can also be used to identify a substance that can associate
 CC with or mediate the biological activity of the proteins. Antibodies can
 CC be used to treat conditions mediated by the kallikrein-like proteins

ALIGNMENTS

26	1352	98.8	258	3	AAB21324	Aab21324 Human EMS
27	1342	98.0	249	3	AAB21307	Aab21307 Human pro
28	1330	97.2	253	3	AAB21308	Aab21308 Human EMS
29	1255	91.7	234	4	AAE00397	Aae000397 Human ser
30	1241	90.7	231	2	AAV25510	Aay25510 Human pro
31	1237	90.4	237	3	AAB21293	Aab21293 Human KLK
32	1205	88.0	449	4	AAM01227	Aam01227 P703P and
33	1205	88.0	449	4	AAM01227	Aau69872 Human pro
34	1205	88.0	449	4	AABU71763	Abu71763 Prostate
35	1205	88.0	449	5	ABB95332	Abb95332 Human P70
36	1205	88.0	449	6	ABR54444	AbR54444 Prostate
37	1205	88.0	449	7	ADB14067	Adb14067 Human pro
38	1205	88.0	449	7	ADG26483	Adg26483 Human pro
39	1205	88.0	585	4	ABU71889	Abu71889 Prostate
40	1205	88.0	585	4	ABU71888	Abu71888 Prostate
41	1205	88.0	585	6	ABR54580	AbR54580 Prostate
42	1205	88.0	585	7	ADB14470	Adb14470 FOPP/hPAP
43	1205	88.0	585	7	ADG26593	Adg26593 Human pro
44	1205	88.0	801	4	ABU71890	Abu71890 Prostate
45	1191	87.0	226	4	AAV72526	Aay72526 Human pro

XX SQ Sequence 254 AA;
Query Match 100.0%; Score 1369; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYRNPRLANDLMLI 120
DB 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYRNPRLANDLMLI 120
QY 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGMPTVLQCVNVSVSEVCSK 180
DB 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQVGPVYTNL 240
DB 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQVGPVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 2

AAU01174
ID AAU01174 standard; protein; 254 AA.

XX AC AAU01174;

DT 04-OCT-2001 (first entry)

DE Human prostate-specific amino acid sequence P703P.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytostatic; gene therapy; metastasis.

OS Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

PF 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;

DR WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.

XX Claim 2; Page 405; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for

CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAU01115 to AAU01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention

XX SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYRNPRLANDLMLI 120

DB 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYRNPRLANDLMLI 120

QY 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGMPTVLQCVNVSVSEVCSK 180

DB 121 KLDSESVESDTIRSIASQCPTAGNSCLVSGWGLLANGMPTVLQCVNVSVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQVGPVYTNL 240

DB 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQVGPVYTNL 240

QY 241 CKFTWIEKTVQAS 254

DB 241 CKFTWIEKTVQAS 254

RESULT 3

AAU69819

ID AAU69819 standard; protein; 254 AA.

XX AC AAU69819;

XX 30-JAN-2002 (first entry)

XX Human prostate cDNA encoded protein #27.

XX Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.

OS Homo sapiens.

XX WO200173032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009919.

XX 27-MAR-2000; 2000US-00536857.

XX 09-MAY-2000; 2000US-00568100.

XX 12-MAY-2000; 2000US-00570737.

XX 13-JUN-2000; 2000US-00593793.

XX 27-JUN-2000; 2000US-00605783.

XX 09-AUG-2000; 2000US-00636215.

XX 29-AUG-2000; 2000US-00651236.

XX 06-SEP-2000; 2000US-00657279.

XX 02-OCT-2000; 2000US-00679426.

XX 10-OCT-2000; 2000US-00685166.

XX 09-NOV-2000; 2000US-00709729.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.

DR N-PSDB; AAS63914.
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.
 XX
 XX Claim 2; Page 405-406; 579pp; English.
 XX The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific polypeptide of the invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
 Db 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
 QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLEADQEPGSMVEASLSVRHPEYNRPLLANDLMLI 120
 Db 61 VHPQWLSAAHCFQNSYTTIGLGLHSLEADQEPGSMVEASLSVRHPEYNRPLLANDLMLI 120
 QY 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
 Db 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 Db 241 CKFTEWIEKTVQAS 254
 RESULT 4
 AAG99059
 ID AAG99059 standard; protein; 254 AA.
 XX
 AC AAG99059;
 XX
 DT 25-SEP-2001 (first entry)
 DE Human prostate-specific amino acid of p703P.
 XX
 KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
 KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
 KW prostate specific antigen; PSA.
 XX
 OS Homo sapiens.
 XX WO200134802-A2.
 PN 17-MAY-2001.
 PD
 XX
 XX 09-NOV-2000; 2000WO-US030904.
 XX
 XX 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-0043686.
 XX
 XX (CORI-) CORIXA CORP.
 PA

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
 XX WPI; 2001-308785/32.
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of
 PT prostate cancer.
 XX
 XX Claim 3; Page 304-305; 325pp; English.
 XX The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1) and
 CC (N1) have cytostatic activity and can be used in vaccine production. The
 CC polypeptides, nucleic acids and antibodies from the present invention are
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
 CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
 CC and polypeptide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
 Db 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
 QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLEADQEPGSMVEASLSVRHPEYNRPLLANDLMLI 120
 Db 61 VHPQWLSAAHCFQNSYTTIGLGLHSLEADQEPGSMVEASLSVRHPEYNRPLLANDLMLI 120
 QY 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
 Db 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 Db 241 CKFTEWIEKTVQAS 254
 RESULT 5
 ABU71710
 ID ABU71710 standard; protein; 254 AA.
 XX
 AC ABU71710;
 XX
 DT 10-JUN-2003 (first entry)
 DE Prostate cancer specific antigen P703P #7.
 XX
 KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX US2002192763-A1.
 PN 19-DEC-2002.
 PD 29-JUN-2001; 2001US-00895793.
 XX

```
XX 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
DR WPI: 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
PS Example 3; SEQ ID NO 525; 85pp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This is the amino acid sequence of a
CC prostate cancer specific antigen. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 254' AA;
Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQWQAALVWENELFCSGYL 60
Db 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQWQAALVWENELFCSGYL 60
QY 61 VHPQWLSAAHCFQNSYTTGLGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTGLGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGMPVLQCVNVSVSSEVCSK 180
Db 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGMPVLQCVNVSVSSEVCSK 180
QY 181 LYDPLYHPMFCAAGGQDQKDSGNGSGGGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPMFCAAGGQDQKDSGNGSGGGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254
XX
RESULT 6
ABB95279
ID ABB95279 standard; protein; 254 AA.
XX
AC ABB95279;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P703P putative full length protein SEQ ID NO 525.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
```

XX WPI; 2002-255649/30.
 XX New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 XX Claim 2; SEQ ID NO 525; 87pp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a
 CC protein described in the invention
 CC
 XX Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 5; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCPHSPQWQAALVMENELFCGVL 60
 DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCPHSPQWQAALVMENELFCGVL 60
 QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
 DB 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
 QY 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 DB 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 DB 181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKTEWIEKTQVAS 254
 DB 241 CKTEWIEKTQVAS 254
 RESULT 7
 ABP54360
 ID ABP54360 standard; protein; 254 AA.
 XX
 XX AC ABP54360;
 XX
 XX 20-JAN-2003 (first entry)
 XX
 XX Human KLK4 protein SEQ ID NO:13.
 XX
 XX Human; KLK4; cancer; benign tumour; cytostatic4.
 XX
 XX Homo sapiens.
 XX
 XX WO200277243-A1.
 XX
 XX 03-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-AU000378.
 XX
 XX 27-MAR-2001; 2001AU-00004022.
 XX
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 XX Dong Y, Clements JA;
 XX
 XX WPI; 2003-029939/02.
 XX
 XX N-PSDB; ABQ83347.
 XX
 XX Detecting the presence or diagnosing the risk of cancer or benign tumor,
 PT e.g. an ovarian, endometrial or prostate cancer, by determining the
 PT presence of or detecting aberrant expression of KLK4 in a biological

PT sample from the patient.
 XX
 XX Disclosure; Page 118-119; 126pp; English.
 XX
 CC The present invention describes a method (M1) for detecting the presence
 CC or diagnosing the risk of cancer or benign tumour in a patient. M1
 CC comprises determining the presence of or detecting aberrant expression of
 CC KLK4 in a biological sample obtained from the patient. KLK4 has
 CC cytostatic activity. The method is useful for detecting the presence or
 CC diagnosing the risk of a cancer or a benign tumour in a patient,
 CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
 CC benign tumour associated with an organ or tissue from the ovaries, or
 CC endometrium or prostate. An agent which can be used for restoring or
 CC modulating KLK4 expression can be used for treating or preventing cancer
 CC or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
 CC molecules from the present invention can be used for detecting aberrant
 CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
 CC cancer or a benign tumour. The present sequence represents human KLK4
 CC from the present invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCPHSPQWQAALVMENELFCGVL 60
 DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCPHSPQWQAALVMENELFCGVL 60
 QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
 DB 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
 QY 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 DB 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 DB 181 LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKTEWIEKTQVAS 254
 DB 241 CKTEWIEKTQVAS 254
 RESULT 8
 ABP54357
 ID ABP54357 standard; protein; 254 AA.
 XX
 XX AC ABP54357;
 XX
 XX 20-JAN-2003 (first entry)
 XX
 XX Human KLK4 protein SEQ ID NO:6.
 XX
 XX Human; KLK4; cancer; benign tumour; cytostatic.
 XX
 XX Homo sapiens.
 XX
 XX WO200277243-A1.
 XX
 XX 03-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-AU000378.
 XX
 XX 27-MAR-2001; 2001AU-00004022.
 XX
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 XX Dong Y, Clements JA;
 XX

DR WPI: 2003-029939/02.
 DR N-PSDB; ABQ83343.
 XX
 PT Detecting the presence or diagnosing the risk of cancer or benign tumor,
 PT e.g. an ovarian, endometrial or prostate cancer, by determining the
 PT presence of or detecting aberrant expression of KLK4 in a biological
 PT sample from the patient.
 XX
 PS Disclosure; Fig 3; 126pp; English.
 XX
 CC The present invention describes a method (M1) for detecting the presence
 CC or diagnosing the risk of cancer or benign tumour in a patient. M1
 CC comprises determining the presence of or detecting aberrant expression of
 CC KLK4 in a biological sample obtained from the patient. KLK4 has
 CC cytotatic activity. The method is useful for detecting the presence or
 CC diagnosing the risk of a cancer or a benign tumour in a patient,
 CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
 CC benign tumour associated with an organ or tissue from the ovaries,
 CC endometrium or prostate. An agent which can be used for restoring or
 CC modulating KLK4 expression can be used for treating or preventing cancer
 CC or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
 CC molecules from the present invention can be used for detecting aberrant
 CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
 CC cancer or a benign tumour. The present sequence represents human KLK4
 CC from the present invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGPWGFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60
 Db 1 MATAGPWGFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60
 QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGQOMVEASLSVRHPEYRNPRLANDLMLI 120
 Db 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGQOMVEASLSVRHPEYRNPRLANDLMLI 120
 QY 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 Db 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKFTWIEKTVQAS 254
 Db 241 CKFTWIEKTVQAS 254
 RESULT 9
 ABR54391
 ID ABR54391 standard; protein; 254 AA.
 XX
 AC ABR54391;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Prostate tumour specific protein sequence SEQ ID 525.
 XX
 KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 KW immune response; prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2002289747-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
 PI Deng T;
 XX
 XX WPI: 2003-167130/16.
 DR
 XX New prostate-specific proteins and genes, useful in gene therapy,
 XX particularly for stimulating an immune response in a patient, or treating
 XX prostate cancer in a patient, as well as for diagnosing prostate cancer
 XX in a patient.
 XX
 XX Example 3; Page 472; 691pp; English.
 PS
 XX The present invention relates to novel prostate-specific proteins (PSP)
 XX and their coding sequences. The PSPs and their coding sequences are
 XX useful for stimulating an immune response in a patient, or for treating
 XX prostate cancer in a patient and for determining, detecting or diagnosing
 XX the presence of a cancer in a patient. The present sequence was used to
 XX illustrate the invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGPWGFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60
 Db 1 MATAGPWGFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60
 QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGQOMVEASLSVRHPEYRNPRLANDLMLI 120
 Db 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGQOMVEASLSVRHPEYRNPRLANDLMLI 120
 QY 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 Db 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKFTWIEKTVQAS 254
 Db 241 CKFTWIEKTVQAS 254
 RESULT 10
 ADB13975
 ID ADB13975 standard; protein; 254 AA.
 XX
 AC ADB13975;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human prostate specific protein P703P.
 XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell.
 XX
 OS Homo sapiens.
 XX

PN US2003185830-A1.
 XX 02-OCT-2003.
 XX 12-NOV-2002; 2002US-00294025.
 XX 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 10-OCT-2000; 2000US-00679426.
 PR 02-NOV-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 PR 09-MAY-2002; 2002US-00144678.
 XX (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 XX
 DR WPI: 2003-756193/71.
 DR N-PSDB; ADBI3974.
 XX
 PT New isolated polypeptide for use in a vaccine for stimulating an immune
 PT response, or for treating or diagnosis cancer, preferably prostate
 PT cancer.
 XX
 PS Example 3; Page; 101pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising no more than
 CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
 CC peptides comprise a fragment ADBI3563 of that contain naturally processed
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
 CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
 CC encoding the proteins and peptides, expression vectors, a host cell
 CC transformed with the vector, an isolated antibody for antigen binding
 CC fragment) that specifically binds to the protein or peptide, detecting
 CC the presence of a cancer in a patient (comprising contacting a patient
 CC sample with a binding agent that binds to the peptides or a polypeptide
 CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
 CC the agent and comparing the amount of polypeptide to a predetermined cut-
 CC off value to determine the presence of cancer), a fusion protein
 CC comprising the peptides or proteins, stimulating or expanding T cells
 CC specific for a tumour protein comprising contacting T cells with the
 CC peptides or the isolated T cell population, treating prostate cancer in a
 CC patient comprising administering a composition comprising the peptides,
 CC nucleic acids, antibodies or compounds, determining the presence of a
 CC cancer in a patient and treating prostate cancer in a patient comprising
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
 CC from a patient with the peptides or antigen presenting cells that express
 CC the peptides so that the T cells proliferate, and administering the
 CC proliferated T cells to the patient. The peptides (or an oligonucleotide

CC that hybridises to nucleic acid encoding them), is used to detect the
 CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
 CC antigen-presenting cells expressing the nucleic acid, are used to
 CC stimulate or expand T cells specific for a tumour protein. The peptides,
 CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
 CC presenting cells are used to stimulate an immune response or treat
 CC prostate cancer in a patient. The present sequence is a prostate specific
 CC protein of the invention. Note: Except where otherwise indicated, the
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=20030185830.

XX Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWAALVMENELFCSGVL 60
 DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWAALVMENELFCSGVL 60
 QY 61 VHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI 120
 DB 61 VHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI 120
 QY 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 DB 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLOGLVSFKGAPCGQGVGVYTNL 240
 DB 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLOGLVSFKGAPCGQGVGVYTNL 240
 QY 241 CKFTIEWIEKTVQAS 254
 DB 241 CKFTIEWIEKTVQAS 254

RESULT 11

ADG26391
 ID ADG26391 standard; protein; 254 AA.
 AC ADG26391;
 XX 26-FEB-2004 (first entry)
 DT 26-FEB-2004 (first entry)
 XX Human prostate-specific polypeptide #60.
 DE Human; prostate-specific polypeptide; prostate cancer; cytostatic.
 KW Homo sapiens.
 OS Homo sapiens.
 XX US2003157089-A1.
 PN 21-AUG-2003.
 PD 09-MAY-2002; 2002US-00144678.
 PF 25-FEB-1997; 97US-00806099.
 XX 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2000US-00759143.
 PR 09-FEB-2001; 2000US-00780669.
 PR 09-MAY-2001; 2000US-00852911.
 PR 29-JUN-2001; 2000US-00895814.
 PR 10-DEC-2001; 2000US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
 PI Meagher MJ, Deng T;
 XX
 WPI; 2003-777973/73.
 DR N-PSDB; ADG26390.
 XX
 PT New polynucleotides encoding prostate specific polypeptides isolated from
 PT a human prostate tumor cDNA library are useful to diagnose and treat
 PT cancer particularly prostate cancer.
 XX
 PS Example 3; SEQ ID NO 525; 99pp; English.
 XX
 CC The invention relates to human prostate-specific polypeptides and the
 CC polynucleotides encoding them. The invention also relates to an isolated
 CC antibody or its antigen-binding fragment that specifically binds a
 CC polypeptide of the invention, a method of detecting cancer in a patient
 CC comprising contacting a biological sample of the patient with an agent
 CC that binds a prostate-specific polypeptide and comparing the amount of
 CC bound polypeptide compared to a predetermined cut-off value and a fusion
 CC protein comprising a prostate-specific polypeptide. The sequences of the
 CC invention are used to diagnose and treat cancer, particularly prostate
 CC cancer. This sequence represents a human prostate-specific polypeptide of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
 DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
 QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 QY 121 KLDSESVESDITIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 DB 121 KLDSESVESDITIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240
 DB 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240
 QY 241 CKFTWIEKTVQAS 254
 DB 241 CKFTWIEKTVQAS 254

RESULT 12
 AAB74830
 ID AAB74830 standard; protein; 1079 AA.
 XX
 AC AAB74830;
 XX
 DT 14-JUN-2001 (first entry)
 XX
 DE Prostate tumour antigen amino acid sequence for a fusion protein.
 XX
 KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KW prostate cancer; immunogenic; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200125272-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US027464.
 XX
 PR 04-OCT-1999; 99US-0157455P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Skeiky YAW, Reed SG, Cheever MA;
 XX
 WPI; 2001-245062/25.
 XX
 PT Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.
 XX
 PS Disclosure; Page 272-276; 276pp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) comprising at
 CC least an immunogenic portion of a prostate tumour antigen protein or its
 CC variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I), prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridise to a polynucleotide
 CC that encodes a prostate specific protein are useful for detecting the
 CC presence or absence of a cancer or monitoring the progression the
 CC progression of a cancer, especially prostate cancer. AAHQ2422 to AAH2872,
 CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1079 AA;

Query Match 100.0%; Score 1369; DB 4; Length 1079;
 Best Local Similarity 100.0%; Pred. No. 3.7e-95;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
 DB 271 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 330
 QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 DB 331 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 390
 QY 121 KLDSESVESDITIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 DB 391 KLDSESVESDITIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 450
 QY 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 240
 DB 451 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL 510
 QY 241 CKFTWIEKTVQAS 254
 DB 511 CKFTWIEKTVQAS 524

RESULT 13

ABU71860
ID ABU71860 standard; protein; 1079 AA.

XX AC ABU71860;

XX DT 10-JUN-2003 (first entry)

XX Prostate specific antigen fusion protein #2.

XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;

XX immunogen; cancer; prostate specific antigen; PSA;

XX prostatic acid phosphatase; PAP; prostate specific membrane antigen;

XX PSMA.

XX Homo sapiens.

XX OS Synthetic.

XX US2002192763-A1.

XX 19-DEC-2002.

XX 29-JUN-2001; 2001US-00895793.

XX 04-OCT-1999; 99US-0157455P.

XX 04-OCT-2000; 2000US-00679272.

XX 28-MAR-2001; 2001US-00822827.

XX (XUJ1/) XU J.

XX (DILL/) DILLON D C.

XX (MITC/) MITCHAM J L.

XX (HARL/) HARLOCKER S L.

XX (JIAN/) JIANG Y.

XX (KALO/) KALOS M D.

XX (FANG/) FANGER G R.

XX (RETT/) RETTER M W.

XX (STOL/) STOLK J A.

XX (DAYC/) DAY C H.

XX (VEDV/) VEDVICK T S.

XX (CART/) CARTER D.

XX (LISX/) LI S X.

XX (WANG/) WANG A.

XX (SKEI/) SKEIKY Y A W.

XX (HEPL/) HEPLER W T.

XX (HEND/) HENDERSON R A.

XX (HURA/) HURAL J P D.

XX (MCNE/) MCNEILL P D.

XX (HOUG/) HOUGHTON R L.

XX (DBAS/) Y DE BASSOLS C V.

XX (FOVT/) FOY T M.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;

XX McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the

XX treatment and diagnosis of prostate cancer.

XX Claim 5; SEQ ID NO 947; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino

XX acid sequence of immunogenic portions of any of the 3 sequences not

XX defined in the specification, or sequences having at least 70 or 90 %

XX sequence identity to any one of the 35 sequences defined in the USPTO web

XX site, which is encoded by any of the 4 nucleotide sequences not defined

XX in the specification. The fusion protein, composition and methods are

XX useful for diagnosing, preventing and/or treating cancer, particularly

XX prostate cancer. The proteins are useful as markers to indicate the

CC presence or absence of cancer. This is the amino acid sequence of a
CC fusion protein of the invention created from fragments of prostate
CC specific antigen (PSA), prostatic acid phosphatase (PAP), prostatic
CC specific membrane antigen (PSMA) and prostate specific antigens of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX

SQ Sequence 1079 AA;

Query Match 100.0%; Score 1369; DB 4; Length 1079;

Best Local Similarity 100.0%; Pred. No. 3.7e-95; Indels 0; Gaps 0;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQQAALVMENELFCSGVL 60

DB 271 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQQAALVMENELFCSGVL 330

QY 61 VHPQWVLSAAHCFQNSYITIGLHSLQADQEPGSMVEASLSVRHPEYNRPRLANDMLI 120

DB 331 VHPQWVLSAAHCFQNSYITIGLHSLQADQEPGSMVEASLSVRHPEYNRPRLANDMLI 390

QY 121 KLDESVSBSDDTIRISISIASQCPTAGNSCLVSGMGLANGRMPTVLQCVNVSVSEVCSK 180

DB 391 KLDESVSBSDDTIRISISIASQCPTAGNSCLVSGMGLANGRMPTVLQCVNVSVSEVCSK 450

QY 181 LYDPLYHPMFCAAGGQDQKSCNDSGGLICNGYLGVSFGKAPCGOVGVGYTNL 240

DB 451 LYDPLYHPMFCAAGGQDQKSCNDSGGLICNGYLGVSFGKAPCGOVGVGYTNL 510

QY 241 CKFTWIEKTVQAS 254

DB 511 CKFTWIEKTVQAS 524

RESULT 14

AAB21320

ID AAB21320 standard; protein; 254 AA.

AC AAB21320;

XX 02-FEB-2001 (first entry)

XX Human prostate.

XX Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; prostate;

XX kallikrein-like protein; serine protease; cytostatic; cancer;

XX Homo sapiens.

XX WO200053776-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-CA000258.

XX 11-MAR-1999; 99US-0124260P.

XX 01-APR-1999; 99US-0127386P.

XX 21-JUL-1999; 99US-0144919P.

XX (MOUN) MOUNT SINAI HOSPITAL.

XX Yousef GM, Diamandis EP;

XX WPI; 2000-587440/55.

XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L

XX protein mediated disorders, especially cancer.

XX Example 4; Fig 17; 184pp; English.

XX

CC The present sequence is human prostate, a member of the serine protease
CC family. Kallikreins and kallikrein-like proteins are a subgroup of the
CC serine protease enzyme family. They catalyze the selective cleavage of
CC specific polypeptide precursors to release peptides with potent
CC biological activity. Nucleic acids encoding kallikrein-like proteins KUK-
CC L1, KUK-L2, KUK-L3, KUK-L4, KUK-L5 and KUK-L6 have been isolated. The
CC proteins are useful in the treatment, monitoring and diagnosis of
CC cancers, especially prostate cancer. They can also be used to identify a
CC substance that can associate with or mediate the biological activity of
CC the proteins. Antibodies can be used to treat conditions mediated by the
CC kallikrein-like proteins
XX

SQ Sequence 254 AA;

Query Match 99.6%; Score 1364; DB 3; Length 254;
Best Local Similarity 99.6%; Pred. No. 2.1e-95;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGYL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDESVSSEDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 15

AA72525
ID AAY72525 standard; protein; 254 AA.
XX
AC AAY72525;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human prostate antigen #3.
XX
KW Human; prostate; p703p; gene therapy; prostate cancer; cytostatic; PIN;
KW prostate intraepithelial neoplasia; NSI; non-structural protein; vaccine;
KW haemagglutinin; prostatic hyperplasia; prostate-specific serine protease;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO200104143-A2.
XX
PD 18-JAN-2001.
XX
PF 11-JUL-2000; 2000WO-EF006618.
XX
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000GB-00015747.
PR 27-JUN-2000; 2000US-00605783.
XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
XX
PI Cabezon Silva T, Dillon DC;
XX
DR WPI; 2001-159380/16.
XX
PT New prostate protein or its fragment linked to a immunological/expression
PT enhancer fusion partner, useful for preparing vaccines for treating
PT prostate cancers or prostate associated tumors.
XX
PS Claim 2; Page 49; 50pp; English.
XX

CC The present protein sequence is a human prostate antigen. The invention
CC relates to a prostate protein (prostate-specific serine protease) or its
CC fragment fused to an immunological or an expression enhancer fusion
CC partner, such as NSI (haemagglutinin). The fusion protein is used for
CC formulating vaccines useful for immunotherapeutically treating patients
CC susceptible to or suffering from prostate-cancer and prostate-expressing
CC tumours other than prostate tumours, prostatic hyperplasia and prostate
CC intraepithelial neoplasia (PIN). Genetic constructs containing prostate
CC nucleic acids are also useful in gene therapy techniques to induce an
CC immune response
XX

SQ Sequence 254 AA;

Query Match 99.6%; Score 1364; DB 4; Length 254;
Best Local Similarity 99.6%; Pred. No. 2.1e-95;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGYL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDESVSSEDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

Search completed: February 10, 2005, 08:51:13
Job time : 167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:37:40 ; Search time 177 Seconds
(without alignments)
734.848 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPMGWFGLYLILGVA.....GVYTNLCKFTWIKTVQAS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1369	100.0	254	1	KLK4 HUMAN
2	1113	81.3	254	2	Q9XSN6
3	1098	80.2	205	2	Q96JE0
4	1087	79.4	205	2	Q96JE2
5	1069.5	78.1	204	2	Q96JE1
6	1010	73.8	255	2	Q9U1S2
7	997.5	72.9	256	2	Q6IE12
8	995	72.7	255	2	Q9Z0M1
9	848	61.9	195	2	Q96PT0
10	845	61.7	159	2	Q96PT1
11	675	49.3	131	2	Q96JD8
12	671	49.0	293	1	KLK5_HUMAN
13	637.5	46.6	293	2	Q9D140
14	577	42.1	146	2	Q96JD7
15	575	42.0	269	2	Q8IU55
16	574	41.9	110	2	Q96RU5
17	569.5	41.6	260	1	NRPN_RAT
18	567.5	41.5	253	1	KLK7_HUMAN
19	563.5	41.2	260	1	NRPN_MOUSE
20	556.5	40.7	253	2	Q8N5N9
21	549	40.1	250	1	KLKE_HUMAN
22	540.5	39.5	242	2	Q7T1R8
23	538.5	39.3	250	2	Q8CGR5
24	537.5	39.3	242	2	Q8QV54
25	537	39.2	276	2	Q8CGR6
26	535.5	39.1	251	1	KLKE_HUMAN
27	534	39.0	246	2	Q6P3Z0
28	533.5	39.0	251	2	Q6B089
29	529.5	38.7	275	2	Q81XD7
30	529	38.6	249	2	Q91VE3
31	527	38.5	250	2	Q63ZF2

32	524	38.3	249	2	Q9QYN4	Q9QYN4 mus musculus
33	524	38.3	261	2	Q29474	Q29474 canis famil
34	524	38.3	276	2	Q9QYN3	Q9QYN3 m hippostas
35	519	37.9	249	2	Q788V0	Q788V0 dissostichu
36	517.5	37.8	277	1	KLKD_HUMAN	Q9UKR3 homo sapien
37	517	37.8	247	2	Q9CPN9	Q9CPN9 m mus muscu
38	516	37.7	235	2	Q63274	Q63274 rattus norv
39	515.5	37.7	260	1	KLK8_HUMAN	Q60259 homo sapien
40	515	37.6	244	1	KLKA_RAT	P36375 rattus norv
41	515	37.6	249	2	Q92046	Q92046 dissostichu
42	513.5	37.5	260	2	Q8IW69	Q8IW69 homo sapien
43	512	37.4	239	2	Q63275	Q63275 rattus norv
44	510.5	37.3	248	1	TRY3_CHICK	Q90629 gallus gall
45	509	37.2	261	1	KLK3_MOUSE	P00756 mus musculus

ALIGNMENTS

RESULT 1	KLK4_HUMAN	STANDARD	PRT;	254 AA.
ID	Q9Y5K2: Q9CZL6; Q9UBJ6;			
AC	16-OCT-2001 (Rel. 40, Created)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Kallikrein-1 precursor (EC 3.4.21.-) (protease) (Kallikrein-like protein 1) (KLK-L1) (Enamel matrix serine proteinase 1).			
DE	Name: KLK4; Synonyms: EMSP1, PRSS17, PSTS;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=99179024; PubMed=10077646; DOI=10.1073/pnas.96.6.3114;			
RX	Nelson P.S., Gan L., Ferguson C., Moss P., Gellinas R., Hood L., Wang K.;			
RT	"Molecular cloning and characterization of prostate, an androgen-regulated serine protease with prostate-restricted expression.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:3114-3119(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=99413477; PubMed=10485467;			
RT	Yousef G.M., Obiezu C.V., Loh L.Y., Black M.H., Diamandis E.P.;			
RT	"Protease/KLK-L1 is a new member of the human kallikrein gene family, is expressed in prostate and breast tissues, and is hormonally regulated.";			
RL	Cancer Res. 59:4252-4256(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;			
RT	Stephenson S.A., Verity A., Ashworth L.K., Clements J.A.;			
RT	"Localization of a new prostate-specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein gene family cluster on chromosome 19q13.3-13.4.";			
RL	J. Biol. Chem. 274:23210-23214(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;			
RT	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepert B., Wang R.;			
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RA	MEDLINE=20323211; PubMed=10891090; DOI=10.1016/S0378-1119(00)00203-1;			
RT	Hu J.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;			
RT	"Characterization of the mouse and human PRSS17 genes, their relationship to other serine proteases, and the expression of PRSS17 in developing mouse incisor.";			
RL	Gene 251:1-8(2000).			

QW	QX	QY	QZ	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100	Q101	Q102	Q103	Q104	Q105	Q106	Q107	Q108	Q109	Q110	Q111	Q112	Q113	Q114	Q115	Q116	Q117	Q118	Q119	Q120	Q121	Q122	Q123	Q124	Q125	Q126	Q127	Q128	Q129	Q130	Q131	Q132	Q133	Q134	Q135	Q136	Q137	Q138	Q139	Q140	Q141	Q142	Q143	Q144	Q145	Q146	Q147	Q148	Q149	Q150	Q151	Q152	Q153	Q154	Q155	Q156	Q157	Q158	Q159	Q160	Q161	Q162	Q163	Q164	Q165	Q166	Q167	Q168	Q169	Q170	Q171	Q172	Q173	Q174	Q175	Q176	Q177	Q178	Q179	Q180	Q181	Q182	Q183	Q184	Q185	Q186	Q187	Q188	Q189	Q190	Q191	Q192	Q193	Q194	Q195	Q196	Q197	Q198	Q199	Q200	Q201	Q202	Q203	Q204	Q205	Q206	Q207	Q208	Q209	Q210	Q211	Q212	Q213	Q214	Q215	Q216	Q217	Q218	Q219	Q220	Q221	Q222	Q223	Q224	Q225	Q226	Q227	Q228	Q229	Q230	Q231	Q232	Q233	Q234	Q235	Q236	Q237	Q238	Q239	Q240	Q241	Q242	Q243	Q244	Q245	Q246	Q247	Q248	Q249	Q250	Q251	Q252	Q253	Q254	Q255	Q256	Q257	Q258	Q259	Q260	Q261	Q262	Q263	Q264	Q265	Q266	Q267	Q268	Q269	Q270	Q271	Q272	Q273	Q274	Q275	Q276	Q277	Q278	Q279	Q280	Q281	Q282	Q283	Q284	Q285	Q286	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299	Q300	Q301	Q302	Q303	Q304	Q305	Q306	Q307	Q308	Q309	Q310	Q311	Q312	Q313	Q314	Q315	Q316	Q317	Q318	Q319	Q320	Q321	Q322	Q323	Q324	Q325	Q326	Q327	Q328	Q329	Q330	Q331	Q332	Q333	Q334	Q335	Q336	Q337	Q338	Q339	Q340	Q341	Q342	Q343	Q344	Q345	Q346	Q347	Q348	Q349	Q350	Q351	Q352	Q353	Q354	Q355	Q356	Q357	Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416	Q417	Q418	Q419	Q420	Q421	Q422	Q423	Q424	Q425	Q426	Q427	Q428	Q429	Q430	Q431	Q432	Q433	Q434	Q435	Q436	Q437	Q438	Q439	Q440	Q441	Q442	Q443	Q444	Q445	Q446	Q447	Q448	Q449	Q450	Q451	Q452	Q453	Q454	Q455	Q456	Q457	Q458	Q459	Q460	Q461	Q462	Q463
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QY 110 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 169
Db 61 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 120

QY 170 VSVSEEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSGFKAPCG 229
Db 121 VSVSEEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSGFKAPCG 180

QY 230 QVGVPGVYTNLCKFTWIEKTVQAS 254
Db 181 QVGVPGVYTNLCKFTWIEKTVQAS 205

RESULT 5
Q96JE1 PRELIMINARY; PRT; 204 AA.
ID Q96JE1
AC Q96JE1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatchi-Glu F.;
RT "Distinct different gene structure of KLK4/KLK-Li/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones.";
RL DNA Cell Biol. 20:435-445 (2001).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF259965; AAK71701.1; -.
DR HSP; P00760; LE2X.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF259965; AAK71701.1; -.
DR HSP; P00760; LE2X.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 204 AA; 21811 MW; 45742165D23A53F3 CRC64;

Query Match 78.1%; Score 1069.5; DB 2; Length 204;
Best Local Similarity 98.5%; Pred. No. 7.7e-87;
Matches 202; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 50 MENELFCSGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYN 109
Db 1 MENELFCSGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYN 60

QY 110 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 169
Db 61 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANG-MPTVLQCVN 119

QY 170 VSVSEEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSGFKAPCG 229
Db 120 VSVSEEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSGFKAPCG 179

QY 230 QVGVPGVYTNLCKFTWIEKTVQAS 254

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Db 180 QVGVPGVYTNLCKFTWIEKTVQAS 204

RESULT 6
Q9JIS2 PRELIMINARY; PRT; 255 AA.
ID Q9JIS2
AC Q9JIS2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
GN Name=Klk4; Synonyms=Prss17;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=20323211; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;
RA Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
RT "Characterization of the mouse and human PRSS17 genes, their
RT relationship to other serine proteases, and the expression of PRSS17
RT in developing mouse incisors";
RL Gene 251:1-8(2000).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF198031; AAF85937.1; -.
DR HSP; P00760; LE2X.
DR MEROPS; S01.251; -.
DR MGD; MGI:1861379; Klk4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 32 255 enamel matrix serine proteinase 1.
SQ SEQUENCE 255 AA; 27536 MW; CBF5FBAF7D4D679C CRC64;

Query Match 73.8%; Score 1010; DB 2; Length 255;
Best Local Similarity 70.1%; Pred. No. 1.9e-81;
Matches 178; Conservative 31; Mismatches 45; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWAAALVMENELFCSGYL 60
Db 2 MYTARTPGWFLGYLILEVTGASASSVSRIIQGDCSPHSQWQAAALFSEDFGFCGVL 61

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYNRPLANDLMLI 120
Db 62 VHPQWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYNRPLANDLMLI 121

QY 121 KLDESVSDDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 122 KLVESVTSNTRISIPVATQPTPDTCVLSGWGQLKNGKLPSSLQCVNLSVASETCRL 181

QY 181 LYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSGFKAPCGQVPGVYTNL 240
Db 182 LYDPLYPHSMFCAGGQDQKDCSCNGDSGGPIVCNRSLOGLVSMGQKCGQPGIPSYTNL 241

QY 241 CKFTWIEKTVQAS 254
Db 242 CKFTWIEKTVQAS 255

RESULT 7
Q6IE12 PRELIMINARY; PRT; 256 AA.
ID Q6IE12

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RESULT 9
Q96PT0 PRELIMINARY; PRT; 195 AA.
AC Q96PT0; MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Kallikrein 4 splice variant.
GN Name=KLK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
RT "Localization of a new prostate-specific antigen-related serine
RT protease gene, KLK4, is evidence for an expanded human kallikrein gene
RT family cluster on chromosome 19q13.3-13.4.";
RL J. Biol. Chem. 274:23210-23214 (1999)
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF148532; AAL14782.1; -;
DR HSSP; Q61955; INPM.
DR GO; GO:0008236; F:serine-type peptidase activity; ISS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; ISS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 195 AA; 20585 MW; EF7E96978B1515B1 CRC64;
Query Match 61.9%; Score 848; DB 2; Length 195;
Best Local Similarity 97.6%; Pred. No. 3.4e-67;
Matches 160; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMENELFCSGYL 60
Db 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITGLHLSLEADQPGSQWVEASLSVRHPEYRPLANDLMLI 120
Db 61 VHPQWVLSAAHCFQNSYITGLHLSLEADQPGSQWVEASLSVRHPEYRPLANDLMLI 120
QY 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANG 164.
Db 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANG 164
RESULT 10
Q96PT1 PRELIMINARY; PRT; 159 AA.
AC Q96PT1; MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Kallikrein 4 splice variant.
GN Name=KLK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
RT "Localization of a new prostate-specific antigen-related serine
RT protease gene, KLK4, is evidence for an expanded human kallikrein gene

RT family cluster on chromosome 19q13.3-13.4.";
RL J. Biol. Chem. 274:23210-23214 (1999)
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF148532; AAL14781.1; -;
DR HSSP; Q61955; INPM.
DR GO; GO:0008236; F:serine-type peptidase activity; ISS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; ISS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 159 AA; 16931 MW; 3CC66BF491B6CA5A CRC64;
Query Match 61.7%; Score 845; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5e-67;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMENELFCSGYL 60
Db 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYITGLHLSLEADQPGSQWVEASLSVRHPEYRPLANDLMLI 120
Db 61 VHPQWVLSAAHCFQNSYITGLHLSLEADQPGSQWVEASLSVRHPEYRPLANDLMLI 120
QY 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANG 159
Db 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANG 159
RESULT 11
Q96JD8 PRELIMINARY; PRT; 131 AA.
AC Q96JD8; MEDLINE=21398046; PubMed=11506707; DOI=10.1098/104454901750361497;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE ARMI (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1098/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-ii/Protease/ARMI
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones";
RL DNA Cell Biol. 20:435-445 (2001).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF259968; AAK71704.1; -;
DR HSSP; Q61955; INPM.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.


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FT CARBOHYD 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 208 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 252 N-linked (GlcNAc...) (Potential).
FT CONFLICT 25 Missing (in Ref. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946 CRC64;

Query Match 49.0%; Score 671; DB 1; Length 293;
Best Local Similarity 45.7%; Pred. No. 2.9e-51;
Matches 134; Conservative 47; Mismatches 72; Indels 40; Gaps 6;

QY 1 MATAGNPMGFLGYLI---LGV-----AGSLVSG----- 26
Db 1 MATAPPPWVLCALITALLGVTEHVLNANDVSCDHPSTNTPSSNQDLGAGAGEDARS 60
QY 27 --SCSQIINGEDCSPHSQPQWAAALVME-NELPCSGVLVHPQWVLSAAHCFQNSYTIIGLG 83
Db 61 DSSSSRIINGSCDMEHTQWQAALLRPNQLYCGAVLHPQWVLLTAACHRCRKPVPFRILGH 120
QY 84 HSLLEADQEPGQOMVEASLSVRHPEYRPLANDMLIKLDESVSESDDTIRISIASOCP 143
Db 121 YSLSPVYESGQOMFGVKSIPHPGVSHPGHSDMLIKLRIRPTKVRPLNVSSHCP 180
QY 144 AGNSCLVSGWGLLANGRM--PTVLQCVNVSVVSEVCSKLYDPLVHPSMFCAGGQDQK 201
Db 181 AGTKCLVSGWGTIKSPQVHFPPKVLQCLNLSVLQKCEDAYPRQIDDTMFCAGDKAGRD 239
QY 202 SCNGDSGGPLICNGYLOGLVSGFKAPCGGVGVGVVTLNCKTEWIEKTVQAS 254
Db 240 SCQDGGPVPVCGNSLQGLVSGWGDYPCARPGRPVGVTNLCRFTKWIQETIQAN 292

RESULT 13
Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:110030019 product:weakly similar to KALLIKREIN 5 (EC
DE 3.4.21.-) (STRATUM CORNEUM TRYPTIC ENZYME) (KALLIKREIN-LIKE PROTEIN 2)
DE (K1K-L2).
GN Name=1110030019Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA the FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

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RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplex capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Koyama T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK003996; BAB23113.1; -.
DR HSP; P00760; 1EZX.
DR MEROPS; S01.418; -.
DR MGD; MGI:1915918; 1110030019Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Query Match 46.6%; Score 637.5; DB 2; Length 293;
Best Local Similarity 41.5%; Pred. No. 2.8e-48;
Matches 122; Conservative 51; Mismatches 80; Indels 41; Gaps 5;

QY 1 MATAGNPMGFLGYLI---LGVAGSLVSG----- 26
Db 1 MATAGHPKWKAMATLITLVLGVSEPLAGDVSSCDNPSGTEPSGTNRDLSTDSKSGDT 60
QY 27 ---SCSQIINGEDCSPHSQPQWAAALVME-NELPCSGVLVHPQWVLSAAHCFQNSYTIIGLG 82
Db 61 RSDSSSRIVNGSDCQKDAQPMQWQALLGPNKLYCGAVLISPQWLLTAACHRCRKPVPFRILG 120
QY 83 LHSLEADQEPGQOMVEASLSVRHPEYRPLANDMLIKLDESVSESDDTIRISIASOCP 142
Db 121 HHSMPVTVESGQOMFGGKISIFHPGVSHPGHSDMLIKLRIRPTKVRPLNVSSHCP 180
QY 143 TAGNSCLVSGWGLL--ANGRMPTVLQCVNVSVVSEVCSKLYDPLVHPSMFCAGGQDQK 200
Db 181 TEGTRCMVSGWGTSTSSSHNNPFPKVLQCLNITVLSEERCCKNSYPGQIDKTMFCA-GDEGR 239
QY 201 DSCNGDSGGPLICNGYLOGLVSGFKAPCGGVGVGVVTLNCKTEWIEKTVQAS 254

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Search completed: February 10, 2005, 08:54:15
Job time : 178 secs

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